AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph beginning at page 2, line 3, as follows:

As used herein, the term ~~Apromoter@~~ "promoter" refers to a nucleic acid sequence which is cable of initiating transcription of a nucleic acid molecule encoding a polypeptide (coding sequence); a ~~Ayeast promoter@~~ "yeast promoter" is capable of initiating transcript of a coding sequence in yeast cells; and ~~Apromoter activity@~~ "promoter activity" refers to the level or amount of transcription initiation of a coding sequence, and encompasses any level above background (*i.e.*, the level or amount that occurs in the absence of a promoter; a background level, which is normally zero).

Please amend the paragraph beginning at page 20, line 15, as follows:

Poly A+ RNA was purified from total RNA using Qiagen Oligotex mRNA Midi Kit (Qiagen, Cat. No. 70042). 2mg of total RNA was used as starting material and made up to a volume of 500μl with DEPC treated H_2O. To this 500μl buffer OBB (2x binding buffer) and 55μl oligotex suspension was added. The ~~AOligotex mRNA Spin-Column Protocol@~~ "Ologotex mRNA Spin Column Protocol" from the kit protocol booklet was followed. The pelleted mRNA was washed in 200μl 75% ethanol, dried and resuspended in 10μl DEPC treated H_2O. Yield of Poly A+ RNA was ~ 8μg for each sample.

Please amend the paragraph beginning at page 23, line 11, as follows:

The hybridization mix comprised: 20μl (11μg) of fragmented cRNA; 2.2μl of control oligo B2 (50pmol/μl) (sequence: ~~5=~~5'Biotin-GTCAAGATGCTACCGTTCAG

~~3=~~3'HPLC purified) (SEQ ID NO:16); 2.2μl Herring Sperm DNA (10mg/ml); 110μl 2x Buffer (2M NaCl, 20mM Tris pH 7.6, 0.01% Triton X-100); and 85.6μl DEPC treated H_2O. The hybridization mix heated to 95°C in a Techne hot block for 5 minutes, followed by incubation at 40°C for 5 minutes. The hybridization mix was clarified by centrifugation in microfuge at 13,000rpm for 5 minutes.

Please amend the paragraph beginning at page 25, line 1, as follows:

Data was collected by scanning the hybridized chips on a Hewlett-Packard GeneArray scanner. A ~~Ahalo@~~"halo" effect (appearance of stain non-specifically across the array image) was seen on one of the scanned images: yeast growing in glucose rich media, sub-set C array. Scanning of this array was aborted after one scan and the chip was washed twice with 200μl 6x SSPE-T and then re-filled as before. This array was then re-scanned three times and the data collected was the average of these three scans. All other arrays were scanned four times without problems and the data collected was the average of the four scans.

Please amend the paragraph beginning at page 25, line 12, as follows:

Based on the *Saccharomyces cerevisiae* genomic sequence in the GenEMBL nucleotide database oligonucleotide primers were designed to amplify the genomic sequence ~~5=~~5' to the following ORFs: YLR110C (Johnston *et al.* (1997) Nature 1997 May 29;387(6632 Suppl):87-90), YMR251WA (common name HOR7) (Bowman *et al.* (1997) Nature May 29;387(6632 Suppl):90-3), YMR107W (Bowman *et al.* (1997) Nature May 29;387(6632 Supl:90-3), and YOL109W (common name ZEO1) (Dujon *et al.*

(1997) Nature May 29;387(6632 Suppl):98-102). The region amplified was the non-coding region separating the selected ORF and the next predicted *Saccharomyces cerevisiae* ORF in the ~~5=~~5' direction, with a minimum length of 500bp.

Please amend the paragraph bridging page 28, line 18, to page 29, line 2 as follows:

The products of the ligations described above were transformed into *E. coli* (~~Invitrogen=s~~ Invitrogen's One-Shot TOP10 Competent cells, cat.no. C4040-10) according to manufacturers protocol. In each case 5μl of the ligation product was added to the cell suspension. The total final cell suspension was plated out onto L-amp plates and incubated overnight at 37°C.

Please amend the paragraph beginning at page 30, line 16, as follows:

Yep13 F2 : CCTCAATTGGATTAGTCTCA – SEQ ID NO:13-aligns to the YEp13 backbone, 290bp ~~5=~~5' of the Hind III site.

Please amend the paragraph beginning at page 30, line 18, as follows:

Luc R1 : CACCTCGATATGTGCATCTG – SEQ ID NO:14- aligns to the Luc ORF, 150bp ~~3=~~ 3'of the NdeI site.

Please amend the paragraph beginning at page 31, line 10, as follows:

All sequences differ by a few base pairs around the ATG, this results from the creation of an NdeI site at the ~~3=~~3'end of the promoter. In addition, the following further alterations from published sequences were identified.

Please amend the paragraph beginning at page 32, line 10, as follows:

pYMR107P+luc: Cloning artifacts created in additional HindIII site and linker to the ~~5=~~5' (*i.e.* outside) of the pYMR107P+luc and promoters:

Please amend the paragraph beginning at page 32, line 16, as follows:

Instead of:

hindIII NotI promoter ~~5=~~5'
AAGCTT-CGCGGCCGCG-NNNNNNN SEQ ID NO:17

The sequence is:

hindIII hindIII NotI promoter ~~5=~~5'
AAGCTT-AGCT-AAGCTT-CGCGGCCGCTG-NNNNNNN SEQ ID NO:18.

Please amend Table 5, beginning at page 34, as follows:

Table 5

Plasmid	Clone number	OD at time of harvesting first 4ml sample	Incubation time at harvesting of first sample (hours)	OD at time of harvesting second 3ml sample
PpPRB1P	7	0.98	24.5	4.80
+luc	8	0.68	28	5.56
	9	1.15	28	5.66
PpYLR110P	8	1.12	28	5.50
+luc	9	0.46	28	4.38
	10	1.16	24.5	5.51
PpYMR251AP	8	1.20	24.5	4.99
+luc	9	1.05	27	4.71
	10	1.15	27	5.18
PpYMR107P	1	1.06	27	5.47
+luc	2	0.49	28.5	4.54
	3	0.97	25.5	5.58
PpZEO1P	1	1.02	28.5	4.84
+luc	2	0.62	28.5	4.97
	3	0.42	28.5	4.31

Please amend Table 6, beginning at page 35, as follows:

Table 6.

Plasmid	Clone number	First sample				Second Sample			
		Readings	(CPS)	Average	Average	Readings	(CPS)	Average	Average
PpPRB1P	7	35890	35690	35790	34898	20322	20975	20648	19867
+luc	8	25498	25276	25387	24495	52997	51778	52388	51607
	9	24137	27797	25967	25075	49192	46971	48081	47300
PpYLR110P	8	52354	53618	52986	52094	41789	38904	40346	39565
+luc	9	105299	99776	102537	101645	85562	84468	85015	84234
	10	107531	109226	108379	107486	22507	22436	22471	21690
PpYMR251AP	8	71993	69797	70895	70003	40869	40202	40536	39755
+luc	9	98853	98389	98621	97729	51159	49828	50493	49712
	10	83210	87546	85378	84485	70091	74576	72334	71553
PpYMR107P	1	9046	8650	8848	6790	29413	28505	28959	28124
+luc	2	3996	4009	4002	1945	24391	23915	24153	23318
	3	3018	3236	3127	1069	23866	23408	23637	22802
PpZEO1P	1	64137	63162	63649	61592	47469	45769	46619	45784
+luc	2	19579	18329	18954	16897	44910	42982	43946	43111
	3	87572	90317	88944	86887	142414	142262	142338	141503

Please amend the paragraph beginning at page 37, line 9, as follows:

The fragments generated by restriction endonuclease digestion of the promoters shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, or SEQ ID NO:4 can be separated by agarose gel electrophoresis. The agarose gel band corresponding to the desired promoter fragment can be cut out of the agarose gel. The fragment can be isolated and purified from the agarose gel by, for example, electroelution or kits such as QIAquick™ gel extraction kit or ~~QIAEX7~~ QIAEX® II Gel Extraction System (Qiagen Cat. No. 28704 and 20021).